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leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS cp45, and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS cp45, said genome or antigenome] combined with one or more heterologous gene(s) or genome segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV genome or antigenome.

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21. (Twice Amended) The chimeric PIV of claim [6] 1, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of attenuating mutations present within HPIV3 JS cp45.

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22. (Twice Amended) The chimeric PIV of claim [6] 1, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of attenuating mutations specifying an amino acid substitution in the L protein at a position corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of in JS *cp*45; in the N protein at a position corresponding to residues Val₉₆ or Ser₃₈₉ of JS cp45, in the C protein at a position corresponding to Ile₉₆ of JS cp45, in the F protein at a position corresponding to residues Ile₄₂₀ or Ala₄₅₀ of JS cp45, in the HN protein at a position corresponding to residue Val₃₈₄ of JS cp45, a nucleotide substitution in a 3' leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS cp45, and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS cp45.

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39. (Twice Amended) An isolated polynucleotide comprising a chimeric parainfluenza virus (PIV) genome or antigenome which includes a partial or complete human parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome [that incorporates at least one and up to a full complement of attenuating mutations present within HPIV3 JS cp45 selected from mutations specifying an amino acid substitution in the L protein at a position corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS *cp*45; in the N protein at a position corresponding to residues Val₉₆ or Ser₃₈₉ of JS *cp*45, in the C protein at a position corresponding to Ile₉₆ of JS cp45, a nucleotide substitution in a 3' leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS cp45, and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS cp45,

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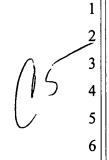
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said genome or antigenome] combined with one or more heterologous gene(s) or genome segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of one or both of HPIV1 and HPIV2 to form a chimeric PIV genome or antigenome.

48. (Twice Amended) A method for producing an infectious attenuated chimeric parainfluenza virus (PIV) particle from one or more isolated polynucleotide molecules encoding said PIV, comprising:

expressing in a cell or cell-free lysate an expression vector comprising an isolated polynucleotide comprising a partial or complete human parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome [that incorporates at least one and up to a full complement of attenuating mutations present within HPIV3 JS *cp*45 selected from mutations specifying an amino acid substitution in the L protein at a position corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS *cp*45; in the N protein at a position corresponding to residues Val₉₆ or Ser₃₈₉ of JS *cp*45, in the C protein at a position corresponding to Ile₉₆ of JS *cp*45, a nucleotide substitution in a 3' leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp*45, and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS *cp*45, said genome or antigenome] combined with one or more heterologous gene(s) or genome segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV genome or antigenome, and PIV N, P, and L proteins.



transcriptional promoter, a polynucleotide sequence which includes a partial or complete human parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome [that incorporates at least one and up to a full complement of attenuating mutations present within HPIV3 JS *cp*45 selected from mutations specifying an amino acid substitution in the L protein at a position corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS *cp*45; in the N protein at a position corresponding to residues Val₉₆ or Ser₃₈₉ of JS *cp*45, in the C protein at a position corresponding to Ile₉₆ of JS *cp*45, a nucleotide substitution in a 3' leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp*45, and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS *cp*45,

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said genome or antigenome] combined with one or more heterologous gene(s) or genome segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV genome or antigenome, and a transcriptional terminator.

Please add new claims 51-52 as follows:

The chimeric PIV of claim 6, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of attenuating mutations present within HPIV3 JS cp45 selected from mutations specifying an amino acid substitution in the L protein at a position corresponding to Tyr942, Leu992, or Thr1558 of JS cp45; in the N protein at a position corresponding to residues Val96 or Ser389 of JS cp45, in the C protein at a position corresponding to Ile96 of JS cp45, a nucleotide substitution in a 3' leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS cp45, and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS *cp*45.

52. The isolated polynucleotide of claim 39, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of attenuating mutations present within HPIV3 JS cp45.--